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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/502,426B

DATE: 05/28/2003
TIME: 15:14:18

Input Set : A:\11696-070001.txt
Output Set: N:\CRF4\05282003\1502426B.raw

ENTERED

RAW SEQUENCE LISTING

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55 tctacaaggc tgtaaccatc tgcaactatt aaattgctt ctttaatgca tctttaacat 1560
 56 atttattgtt agttggatt taataagagc gaacttgtaa cattacaata ttatattag 1620
 57 atactagtat gtgattattc caaatacata ctttggatgt ttaaactaa tcttgttct 1680
 58 tcctacggta taaatattaa tcatcgaggt aaaaaaaagtt ttgtcttatt ttcgcgatgc 1740
 59 atgaaggata aacctaatga cttaatttt ttgaaaatgt aacccttta ctcatagatt 1800
 60 aattaccgtt tggtttgtt gccataatga cagcctctac aactgtgata gtcaattttt 1860
 61 tctgcaaata ttaaatttagg aattcaatgc tactatcaat agaagaaaaca gctgagttt 1920
 62 acattttaat ttaaagacaa aattttgaa aaatgttata atttctaaca atattattaa 1980
 63 aatatgatgc ctataatgtt ttcctatgt tcttaaaaata tttttttta tatttagtta 2040
 64 taaatacatt atgaaccaat aatagttgtt gaattcaaat atctccatta atatttttg 2100
 65 aaatctacaa attattaata tttagtcaat aacaatgcat agaaaagtcc aaaaaaaatt 2160
 66 ttgttaacag aaacttccaa attttttttt tttatggAAC aagaaataac agatagaaaa 2220
 67 ctatttgtt gtggaatggA agtagtaata tacattaagc aaattttaaa aaatttatata 2280
 68 agcctatacg cgctcaaagt atgttatcta gttaggtgaa ttaataatgc atggtgcat 2340
 69 tcagaattgg gacaacaatg aaaacggaaat taaaatatta actttaaaat aaataaaaaat 2400
 70 ttgagtaaat gtgtttctg actattgagg ggcaaaaaaa agacaatgcc aaaagtctac 2460
 71 gggtttgact gtccagttcg gtaataatct aataactctg tctttgaccg cacgctcgtg 2520
 72 taggggtcct tctgacattt tcactgttct acccctactc gtgagccac cctttccca 2580
 73 tattctaagg gtaattttgg aaatcccaat ttaaaccgat tgagaccgta ccggacttcc 2640
 74 tgggattctg ctggagcatt tatcaaaaat tattagcagc aatgggttta ttaattttaa 2700
 75 aactcacaac ttgatcagat aaaattcat aaacactttt acgatggatt cgtacgatct 2760
 76 atctaatttttctt ctaccacggtt ggtatggaaat tatagtacta tttagccagag 2820
 77 acaatttgatt atagatataat ccattaatcc atgatattta tgatataaat agctgtttaa 2880
 78 ctatccagc atcgcagctt tctgcaactt ttgttttaa ttaagagtt taataaataa 2940
 79 aagtattaaa aggagcataa cgaggcaaca aaagtaatga acacggagaa acaaagcca 3000
 80 tgaagctcat tggtagttt aagcttaata agaagattttt attaaattttt aatgacgatg 3060
 81 ataacaatatttttctgat cttctttaaa acccccttctt acaaacagaa gctccctttt 3120
 82 tcagtagaaat tccgattccc aatcttaaag acaaagccat tagaaagagaa aagttagtga 3180
 83 gagagagaga gaaacttagct ccatgttgcg aacagagcat catactctt tacctcttct 3240
 84 tcttcctccca tcgctttgtt ctcttcttctt cttcttgatt ctcttgcgaa gaagaaatag 3300
 85 aaaaaaccaga ttcaatctac ctccgggtaa atccgggtgg ccatttcttgc tgaaaccat 3360
 86 cggttatctt aaaccgtaca ccggccacaac actcggtgac ttcatgcaac aacatgtctc 3420
 87 caagtaaaca acaacatctt ccaaaaactc aaaaaaaataa atcctcttgc tttgaaatttt 3480
 88 gactaatgtt gtttatttttca caggtatggt aagatataat gatcgactt gtttggagaa 3540
 89 ccaacgatcg tatcagctga tgctggactt aatagattca tattacaaaa cgaagggagg 3600
 90 ctctttgaat gtagttatcc tagaagtata ggtgggattc ttggaaatg gtcgtatgtt 3660
 91 gttcttgggtt gtgacatgca tagagatatg agaagatctt cgtttaactt cttaagtac 3720
 92 gcaacgtctta gaactattctt acttaaagat gttgagagac atactttgtt tgttcttgat 3780
 93 tcttggcaac aaaactctat tttctctgtt caagacgagg ccaaaaaaggt ttttattttt 3840
 94 atcttttattt ttgtctaaatt tttttgttta tgaatcttta gagtttctaa cttttttttt 3900
 95 ttaattgaa cagtttacgt ttaatctttaat ggcgaagcat ataatgagta tggatcctgg 3960
 96 agaagaagaa acagagcaat taaagaaaga gtatgtactt ttcatgaaag gagttgtctc 4020
 97 tgctcctcta aatctaccag gaactgctta tcataaagctt cttcaggatc atttattttt 4080
 98 ttttgcgttta aagtccacaaat ctctcattt aggtttttaa ttttattttt tttttttttt 4140
 99 aaaaatatcta aaatgggttgtt gtagtcacga gcaacgatataat tgaagttcat tgagggaaa 4200
 100 atgaaagaga gaaaatttggaa tatcaaggaa gaagatcaag aagaagaaga agtggaaaaca 4260
 101 gaggatgaag cagagatgag taagagtgtt catgttagga aacaaagaac agacgatgtt 4320
 102 cttttggat gggttttgaa acattcgaat ttatcgacgg agcaaaatctt cgtatctt 4380
 103 cttagttgtt tatttgcgg acatgagact tcttctgttgc ccatttgcgtt cgtatctt 4440

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155	20	25	30	
156	Arg Lys Thr Arg Phe Asn Leu Pro Pro Gly Lys Ser Gly Trp Pro Phe			
157	35	40	45	
158	Leu Gly Glu Thr Ile Gly Tyr Leu Lys Pro Tyr Thr Ala Thr Thr Leu			
159	50	55	60	
160	Gly Asp Phe Met Gln Gln His Val Ser Lys Tyr Gly Lys Ile Tyr Arg			
161	65	70	75	80
162	Ser Asn Leu Phe Gly Glu Pro Thr Ile Val Ser Ala Asp Ala Gly Leu			
163	85	90	95	
164	Asn Arg Phe Ile Leu Gln Asn Glu Gly Arg Leu Phe Glu Cys Ser Tyr			
165	100	105	110	
166	Pro Arg Ser Ile Gly Gly Ile Leu Gly Lys Trp Ser Met Leu Val Leu			
167	115	120	125	
168	Val Gly Asp Met His Arg Asp Met Arg Ser Ile Ser Leu Asn Phe Leu			
169	130	135	140	
170	Ser His Ala Arg Leu Arg Thr Ile Leu Leu Lys Asp Val Glu Arg His			
171	145	150	155	160
172	Thr Leu Phe Val Leu Asp Ser Trp Gln Gln Asn Ser Ile Phe Ser Ala			
173	165	170	175	
174	Gln Asp Glu Ala Lys Lys Phe Thr Phe Asn Leu Met Ala Lys His Ile			
175	180	185	190	
176	Met Ser Met Asp Pro Gly Glu Glu Thr Glu Gln Leu Lys Lys Glu			
177	195	200	205	
178	Tyr Val Thr Phe Met Lys Gly Val Val Ser Ala Pro Leu Asn Leu Pro			
179	210	215	220	
180	Gly Thr Ala Tyr His Lys Ala Leu Gln Ser Arg Ala Thr Ile Leu Lys			
181	225	230	235	240
182	Phe Ile Glu Arg Lys Met Glu Glu Arg Lys Leu Asp Ile Lys Glu Glu			
183	245	250	255	
184	Asp Gln Glu Glu Glu Val Lys Thr Glu Asp Glu Ala Glu Met Ser			
185	260	265	270	
186	Lys Ser Asp His Val Arg Lys Gln Arg Thr Asp Asp Asp Leu Leu Gly			
187	275	280	285	
188	Trp Val Leu Lys His Ser Asn Leu Ser Thr Glu Gln Ile Leu Asp Leu			
189	290	295	300	
190	Ile Leu Ser Leu Leu Phe Ala Gly His Glu Thr Ser Ser Val Ala Ile			
191	305	310	315	320
192	Ala Leu Ala Ile Phe Phe Leu Gln Ala Cys Pro Lys Ala Val Glu Glu			
193	325	330	335	
194	Leu Arg Glu Glu His Leu Glu Ile Ala Arg Ala Lys Lys Glu Leu Gly			
195	340	345	350	
196	Glu Ser Glu Leu Asn Trp Asp Asp Tyr Lys Lys Met Asp Phe Thr Gln			
197	355	360	365	
198	Cys Val Ile Asn Glu Thr Leu Arg Leu Gly Asn Val Val Arg Phe Leu			
199	370	375	380	
200	His Arg Lys Ala Leu Lys Asp Val Arg Tyr Lys Gly Tyr Asp Ile Pro			
201	385	390	395	400
202	Ser Gly Trp Lys Val Leu Pro Val Ile Ser Ala Val His Leu Asp Asn			
203	405	410	415	

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204 Ser Arg Tyr Asp Gln Pro Asn Leu Phe Asn Pro Trp Arg Trp Gln Gln
205 420 425 430
206 Gln Asn Asn Gly Ala Ser Ser Ser Gly Ser Gly Ser Phe Ser Thr Trp
207 435 440 445
208 Gly Asn Asn Tyr Met Pro Phe Gly Gly Gly Pro Arg Leu Cys Ala Gly
209 450 455 460
210 Ser Glu Leu Ala Lys Leu Glu Met Ala Val Phe Ile His His Leu Val
211 465 470 475 480
212 Leu Lys Phe Asn Trp Glu Leu Ala Glu Asp Asp Gln Pro Phe Ala Phe
213 485 490 495
214 Pro Phe Val Asp Phe Pro Asn Gly Leu Pro Ile Arg Val Ser Arg Ile
215 500 505 510
216 Leu
219 <210> SEQ ID NO: 3
220 <211> LENGTH: 24
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Primer: D4OVERF
227 <400> SEQUENCE: 3
228 atgttcgaaa cagagcatca tact 24
230 <210> SEQ ID NO: 4
231 <211> LENGTH: 21
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Primer: D4PRM
238 <400> SEQUENCE: 4
239 cctcgatcaa agagagagag a 21
241 <210> SEQ ID NO: 5
242 <211> LENGTH: 29
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Primer: D4RTF
249 <400> SEQUENCE: 5
250 ttcttggtga aaccatcggt tatctaaa 29
252 <210> SEQ ID NO: 6
253 <211> LENGTH: 26
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Primer: D4RTR
260 <400> SEQUENCE: 6
261 tatgataagc agttcctggc agattt 26
263 <210> SEQ ID NO: 7
264 <211> LENGTH: 21
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/502,426B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:25; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,42,43,46
Seq#:25; Xaa Pos. 48,50,56,57,58,61,62,63,64,65,66,67,68,72,82,92,93,94,95
Seq#:25; Xaa Pos. 96,97,102,107,108,111,112,113,114,126,128,136,138,142,146
Seq#:25; Xaa Pos. 148,149,153,154,156,160,163,165,166,168,175,178,180,183
Seq#:25; Xaa Pos. 184,185,186,190,193,197,201,203,204,206,207,208,209,212
Seq#:25; Xaa Pos. 213,216,217,218,219,221,228,229,230,232,233,236,237,239
Seq#:25; Xaa Pos. 240,242,244,245,246,247,250,252,254,268,272,276,281,282
Seq#:25; Xaa Pos. 284,287,288,289,290,291,292,293,294,295,296,298,300,302
Seq#:25; Xaa Pos. 306,307,308,309,310,311,312,313,314,315,316,317,318,319
Seq#:25; Xaa Pos. 320,321,322,323,324,325,326,334,336,337,338,339,340,341
Seq#:25; Xaa Pos. 345,346,347,348,352,355,357,359,360,372,374,375,381,387
Seq#:25; Xaa Pos. 389,395,398,403,404,405,408,411,412,418,421,432,437,440
Seq#:25; Xaa Pos. 442,451,459,471,481,484,485,487,488,489,490,494,495,496
Seq#:25; Xaa Pos. 497,498,499,500,501,502,503,505,506,526,535,541,542,543
Seq#:25; Xaa Pos. 545,546,547,551,555,558,566,567,570,571,572,573,574,575
Seq#:26; Xaa Pos. 4,8,10
Seq#:28; Xaa Pos. 1,13,15,16